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RAW SEQUENCE LISTING   DATE: 11/01/2001
PATENT APPLICATION: US/09/700,813   TIME: 09:59:12

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 3 <110> APPLICANT: SIERRA-HONIGMANN, Rocio
 5 <120> TITLE OF INVENTION: MODULATION OF ANGIOGENESIS AND WOUND HEALING
 7 <130> FILE REFERENCE: 044574-5029
 9 <140> CURRENT APPLICATION NUMBER: US 09/700,813
10 <141> CURRENT FILING DATE: 1999-05-20
12 <150> PRIOR APPLICATION NUMBER: PCT/US99/11209
13 <151> PRIOR FILING DATE: 1999-05-20
15 <150> PRIOR APPLICATION NUMBER: US 60/086,354
16 <151> PRIOR FILING DATE: 1998-05-28
18 <160> NUMBER OF SEQ ID NOS: 21
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3656
24 <212> TYPE: DNA
25 <213> ORGANISM: Mus musculus
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32 ggaatttctt tatgtgatag ctgcacttaa cctggcatat ccaatctctc cctggaaatt     180
34 taagttgttt tgtggaccac cgaacacaac cgatgactcc tttctctcac ctgctggagc     240
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46 gaattatgac tctaaggtcc atcttttata tgatctgcct gaagtcatag atgattcgcc     600
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58 agagaattct acaattgtaa gagaggctgc tgaaattgtc tcagctacat ctctgctggt     960
60 agacagtgtg cttcctggat cttcatatga ggtccaggtg aggagcaaga gactggatgg    1020
62 ttcaggagtc tggagtgact ggagttcacc tcaagtcttt accacacaag atgttgtgta    1080
64 ttttccaccc aaaattctga ctagtgttgg atcgaatgct tcttttcatt gcatctacaa    1140
66 aaacgaaaac cagattatct cctcaaaaca gatagtttgg tggaggaatc tagctgagaa    1200
68 aatccctgag atacagtaca gcattgtgag tgaccgagtt agcaaagtta ccttctccaa    1260
70 cctgaaagcc accagacctc gagggaagtt tacctatgac gcagtgtact gctgcaatga    1320
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84 aaaaccacta cctccatcta acgtaaaagc agagattact gtaaacactg gattattgaa    1740
86 agtatcttgg gaaaagccag tctttccgga gaataacctt caattccaga ttcgatatgg    1800
88 cttaagtgga aaagaaatac aatggaagac acatgaggta ttcgatgcaa agtcaaagtc    1860
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 94 tgtaaaagtt cctatgagag ggcctgaatt ttggagaaaa atggatgggg acgttactaa   2040
 96 aaaggaqaga aatgtcacct tgctttggaa gcccctgacg aaaaatgact cactgtgtag   2100
 98 tgtgaggagg tacgtggtga agcatcgtac tgcccacaat gggacgtggt cagaagatgt   2160
100 gggaaatcgg accaatctca ctttcctgtg gacagaacca gcgcacactg ttacagttct   2220
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114 gcagcagaat gacgcagggc tgtatgtcat tgtacccata attatttcct cttgtgtcct   2640
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144 gaactttgta ccttacatgc cccaatttca aacctgttcc acgcacagtc acaagataat   3540
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153 <212> TYPE: PRT
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161 Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
162             20              25              30
164 Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
165         35              40              45
167 Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
168     50              55              60
170 Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
171 65              70              75              80
173 Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
174             85              90              95
176 Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
177         100             105             110
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182 Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Ile Ile Cys His Met
183     130             135             140
185 Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
186 145             150             155             160
188 Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
189             165             170             175
191 Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
192             180             185             190
194 Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
195             195             200             205
197 Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
198     210             215             220
200 Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
201 225             230             235             240
203 Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
204             245             250             255
206 Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
207             260             265             270
209 Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
210     275             280             285
212 Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
213     290             295             300
215 Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
216 305             310             315             320
218 Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
219             325             330             335
221 Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
222             340             345             350
224 Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
225             355             360             365
227 Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
228     370             375             380
230 Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
231 385             390             395             400
233 Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
234             405             410             415
236 His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
237             420             425             430
239 Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
240             435             440             445
242 Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
243     450             455             460
245 His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
246 465             470             475             480
248 Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
249             485             490             495
251 Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
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252              500              505              510
254 Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
255          515              520              525
257 Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
258          530              535              540
260 Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
261 545              550              555              560
263 Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
264              565              570              575
266 Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
267          580              585              590
269 Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
270          595              600              605
272 Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
273          610              615              620
275 Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
276 625              630              635              640
278 Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
279              645              650              655
281 Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
282          660              665              670
284 Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
285          675              680              685
287 Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
288          690              695              700
290 Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
291 705              710              715              720
293 Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
294              725              730              735
296 Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
297          740              745              750
299 Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
300          755              760              765
302 Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
303          770              775              780
305 Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
306 785              790              795              800
308 Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
309              805              810              815
311 Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp
312          820              825              830
314 Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile
315          835              840              845
317 Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
318          850              855              860
320 Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
321 865              870              875              880
323 Trp Ala Gln Gly Leu Asn Phe Gln Lys Pro Glu Thr Phe Glu His Leu
324              885              890              895
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326 Phe Thr Lys His Ala Glu Ser Val Ile Phe Gly Pro Leu Leu Leu Glu
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329 Pro Glu Pro Ile Ser Glu Glu Ile Ser Val Asp Thr Ala Trp Lys Asn
330         915             920             925
332 Lys Asp Glu Met Val Pro Ala Ala Met Val Ser Leu Leu Leu Thr Thr
333         930             935             940
335 Pro Asp Pro Glu Ser Ser Ser Ile Cys Ile Ser Asp Gln Cys Asn Ser
336 945             950             955             960
338 Ala Asn Phe Ser Gly Ser Gln Ser Thr Gln Val Thr Cys Glu Asp Glu
339             965             970             975
341 Cys Gln Arg Gln Pro Ser Val Lys Tyr Ala Thr Leu Val Ser Asn Asp
342         980             985             990
344 Lys Leu Val Glu Thr Asp Glu Glu  Gln Gly Phe Ile His  Ser Pro Val
345         995             1000            1005
347 Ser Asn  Cys Ile Ser Ser Asn  His Ser Pro Leu Arg  Gln Ser Phe
348     1010            1015            1020
350 Ser Ser  Ser Ser Trp Glu Thr  Glu Ala Gln Thr Phe  Phe Leu Leu
351     1025            1030            1035
353 Ser Asp  Gln Gln Pro Thr Met  Ile Ser Pro Gln Leu  Ser Phe Ser
354     1040            1045            1050
356 Gly Leu  Asp Glu Leu Leu Glu  Leu Glu Gly Ser Phe  Pro Glu Glu
357     1055            1060            1065
359 Asn His  Arg Glu Lys Ser Val  Cys Tyr Leu Gly Val  Thr Ser Val
360     1070            1075            1080
362 Asn Arg  Arg Glu Ser Gly Val  Leu Leu Thr Gly Glu  Ala Gly Ile
363     1085            1090            1095
365 Leu Cys  Thr Phe Pro Ala Gln  Cys Leu Phe Ser Asp  Ile Arg Ile
366     1100            1105            1110
368 Leu Gln  Glu Arg Cys Ser His  Phe Val Glu Asn Asn  Leu Ser Leu
369     1115            1120            1125
371 Gly Thr  Ser Gly Glu Asn Phe  Val Pro Tyr Met Pro  Gln Phe Gln
372     1130            1135            1140
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390 ccaaaaccct catcaagacc attgtcacca ggatcaatga catttcacac acgcagtcgg   180
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398 tggccttctc caagagctgc tccctgccgc agacccgtgg cctgcagaag ccagagagcc   420
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